

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2003, 06:15:48 ; Search time 2313 Seconds

(without alignments)
10502.910 Million cell updates/sec

Title: US-09-043-944-5

Perfect score: 1500

Sequence: 1 gtttaattcccaagtttga.....taaaaaaaaaaaaaaaaaaaaaa 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	31.4	477	13	B1174328
2	374	24.9	386	13	B1175258
3	362	24.1	374	14	C66636
4	361.4	24.1	375	14	C47805
5	360	24.0	360	9	AV190680
6	350.6	23.4	360	9	AV186436

ALIGNMENTS

7	350	23.3	360	9	AV198059
8	342.6	22.8	374	9	AV192017
9	340.6	22.7	360	14	C39939
c 10	287	19.1	300	9	AV185173
c 11	286	19.1	300	14	C29641
c 12	285	19.0	300	14	C55887
c 13	283.4	18.9	300	9	AV178913
c 14	280.8	18.7	300	14	C29851
c 15	276.4	18.4	300	14	C35957
c 16	272.6	18.2	300	14	C34382
c 17	268.8	17.9	300	9	AV175978
c 18	253.6	16.9	300	9	AV179958
c 19	221.8	14.8	1101	13	BM548100
20	219	14.6	661	9	AI675803
21	217.4	14.5	703	9	AI925372
22	216.8	14.5	1998	11	AK014706
23	212.6	14.2	680	9	AI831581
24	207.8	13.9	1006	9	AL553513
25	205.2	13.7	977	9	AL553084
26	204.2	13.6	705	10	AW604230
27	204.2	13.6	733	10	AW850631
28	203.8	13.6	613	10	AW367465
29	203.2	13.5	640	10	AW604295
30	202.6	13.5	671	10	AW850640
31	202.6	13.5	714	10	AW604310
32	202.6	13.5	735	10	AW850636
33	202.2	13.5	573	10	AW850727
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36	201.4	13.4	593	10	AW850573
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42	198.8	13.3	591	10	AW850561
43	198.6	13.2	588	10	AW367429
44	198.4	13.2	605	12	BF334085
45	198.2	13.2	570	10	AW850715
46	197.8	13.2	614	10	AW850639
47	196.8	13.1	584	10	AW376998
48	191.6	12.8	601	10	AW604233
49	190.4	12.7	590	10	AW367487
50	189.4	12.6	553	10	AW367418
51	188.8	12.6	827	12	BG288033
52	188.6	12.6	545	10	AW604271
53	187.6	12.5	544	10	AW850719
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55	184.8	12.3	587	9	AA993681
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57	184.4	12.3	544	10	AW850723
58	183.4	12.2	544	10	AW604272
59	182.6	12.2	551	10	AW376886
60	182.2	12.1	704	12	BG633935
c 61	181.4	12.1	689	10	AW752758
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63	180.8	12.1	660	10	AW850564
64	180.6	12.0	545	10	AW752760
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68	175.8	11.7	561	10	AW367547
c 69	175.6	11.7	646	10	AW752778
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c 71	174.8	11.7	654	10	AW376926
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c 73	172.6	11.5	555	10	AW367563
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c 75	171.6	11.4	994	9	AL555434

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C29851	C29851
C35957	C35957
C34382	C34382
AV175978	AV175978
AV179958	AV179958
BM548100	BM548100
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AI925372	AI925372
AK014706	AK014706
AI831581	AI831581
AL553513	AL553513
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AW850640	AW850640
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AW604307	AW604307
AW850572	AW850572
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AW604272	AW604272
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AW752758	AW752758
AW376995	AW376995
AW850564	AW850564
AW752760	AW752760
AW850571	AW850571
BE283320	BE283320
AW752766	AW752766
AW367547	AW367547
AW752778	AW752778
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BI174328
477 bp mRNA linear EST 09-JUL-2001
OSTF019E11_1 AD-wrmcDNA Caenorhabditis elegans cdna similar to
AAD50991, mRNA sequence.
BI174328
BI174328.1 GI:14640131
EST.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 477)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I.T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@fci.harvard.edu or
philippe_vaglio@fci.harvard.edu
POLYA-No.
LOCATION/Qualifiers
1. .477
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 131 a 87 c 109 g 150 t
ORIGIN
Query Match 31.4%; Score 470.6; DB 13; Length 477;
Best Local Similarity 99.2%; Pred. No. 7.7e-72;
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 41 AACAGGAGCGGAGGTGCAGATCGCGAACAACATACCGTTACGGTACAAATCTGATAA 100
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Db 1 AACAGGAGCGGAGGTGCAGATCGCGAACAACATACCGTTACGGTACAAATCTGATAA 60
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QY 101 CAATCCGAATAGCCAAAGACGAGAAATGTTGTGGAAGAGCGGAGCTGAAATACGGAG 160
|||||
Db 61 CAATCCGAATAGCCAAAGACGAGAAATGTTGTGGAAGAGCGGAGCTGAAATACGGAG 120
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QY 161 CATCTCAGCTTATCATCTATTTGTGCGGTGTCACATATGCATGCGTCTGTTGTTTAA 220
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Db 121 CATCTCAGCTTATCATCTATTTGTGCGGTGTCACATATGCATGCGTCTGTTGTTTAA 180
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QY 221 CGATGACAGCATACGTTTTATAGTCAAAACAATGGAAGCATTTACTATCATACCTTT 280
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Db 181 CGATGACAGCATACGTTTTATAGTCAAAACAATGGAAGCATTTACTATCATACCTTT 240
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QY 281 TTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACCTTGGAAATGCTCTCG 340
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241 TTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACCTTGGAAATGCTCTCG 300
QY 341 TCATGTTGTGCGGTGCTTCTGATGACAGTCTGCTGATGTTTCTATAATAACAAGT 400
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QY 401 TTTATAAGCTTATTCATGATGATGCTTATTCAGCAGTCTTCTCTCTCTCTCTCTCT 460
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Db 361 TTTATAAGCTTATTCATGATGATGCTTATTCAGCAGTCTTCTCTCTCTCTCTCTCT 420
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QY 461 CTCAATCTATGTCGAAGAAGTCTGAAAAGTTTCGATGTTCCAGCGCAGTAT 517
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Db 421 CTCAATCTATGTCGAAGAAGTCTGAAAAGTTTCGATGTTCCAGCGCAGTAT 477
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BI175258
386 bp mRNA linear EST 09-JUL-2001
OSTR019E11_1 AD-wrmcDNA Caenorhabditis elegans cdna similar to
AAD50991, mRNA sequence.
BI175258
BI175258.1 GI:14641061
EST.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 386)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I.T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@fci.harvard.edu or
philippe_vaglio@fci.harvard.edu
POLYA-No.
LOCATION/Qualifiers
1. .386
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 108 a 82 c 100 g 96 t
ORIGIN
Query Match 24.9%; Score 374; DB 13; Length 386;
Best Local Similarity 99.7%; Pred. No. 4.2e-55;
Matches 385; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 937 AAAGTGAACGAATTCCTCAAAAAGTGAATCGAATCGAATCTAGCTTCAACGACA 996
|||||
Db 386 AAAGTGAACGAATTCCTCAAAAAGTGAATCGAATCGAATCTAGCTTCAACGACA 327
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QY 997 CAAAACCTGGAGTAAGGTTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGAC 1056
Db 326 CAAAACCTGGAGTAAGGTTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGAC 267
QY 1057 GCCAATTTTCACAGGCACCAAGAGGAGAGAGAGGTGTGAACTTGGTCTGGCGACTTC 1116
Db 266 GCCAATTTTCACAGGCACCAAGAGGAGAGAGAGGTGTGAACTTGGTCTGGCGACTTC 207
QY 1117 ATTTTCTACTCTGTTCTCTCGGCAAGGCTTATCGTACTTTTACGTGGAACACGACTATC 1176
Db 206 ATTTTCTACTCTGTTCTCTCGGCAAGGCTTATCGTACTTTTACGTGGAACACGACTATC 147
QY 1177 GCTTGTATGTGGCCATTTCTATCGTCTCTGCTTCACTCTGCTGCTGCTGCTGCTGCTTC 1236
Db 146 GCTTGTATGTGGCCATTTCTATCGTCTCTGCTTCACTCTGCTGCTGCTGCTGCTGCTTC 87
QY 1237 AAACGAGCACTCCCGGCTCTG-CAATTTCCATTTCTCCGGACTCAATTTTACTTTTGT 1295
Db 86 AAACGAGCACTCCCGGCTCTGCAATTTCCATTTCTCCGGACTCAATTTTACTTTTGT 27
QY 1296 ACCCGCTGGATCATCCCCCATTTGT 1321
Db 26 ACCCGCTGGATCATCCCCCATTTGT 1

RESULT 3
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LOCUS 374 bp mRNA linear EST 22-SEP-1997
DEFINITION C66636 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
ACCESSION C66636
VERSION C66636.1 GI:2425566
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS Kohara,Y., Mochizuki,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
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/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(el489)"
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Best Local Similarity 99.7%; Pred. No. 5.1e-53;
Matches 373; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 278 CTTTGTCCGGGAACACAGACATATCGTTGAGAGGAGTTGATGTCACATTGG-AAATGCT 336
Db 1 CTTTGTCCGGGAACACAGACATATCGTTGAGAGGAGTTGATGTCACATTGGNAATGCT 60
QY 337 CTGCTATGTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
Db 61 CTGCTATGTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

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QY 397 AAGTTTTATAAGCTTATTCATGATGGCTTATGTGTCAGCAGTTTTCTTCTTTTCCCTA 456
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QY 457 TTCACATACATCTATGTCGAAGAAGTTCTGAAAAGTTTCGATGTGTCCTCCAGCGCACTA 516
Db 181 TTCACATACATCTATGTCGAAGAAGTTCTGAAAAGTTTCGATGTGTCCTCCAGCGCACTA 240
QY 517 TTGGTTTTTTTGGAGCTGGTACTATGAGTTCTCGAATGATGTATACATTCGAA 576
Db 241 TTGGTTTTTTTGGAGCTGGTACTATGAGTTCTCGAATGATGTATACATTCGAA 300
QY 577 GTTCATTCGCTGTCGAACAGTTCTACCTTATTACAAATGTCGCACTAATGGCTCTGGTC 636
Db 301 GTTCATTCGCTGTCGAACAGTTCTACCTTATTACAAATGTCGCACTAATGGCTCTGGTC 360
QY 637 TTTATCAAGTACCT 650
Db 361 TTTATCAAGTACCT 374

RESULT 4
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LOCUS 375 bp mRNA linear EST 18-OCT-1999
DEFINITION C47805 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
ACCESSION C47805
VERSION C47805.1 GI:2384058
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS Kohara,Y., Mochizuki,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

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Matches 373; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 921 AACGCCAAACAGCCCAAGTGAACGAATTCCTCAAAAAGTCCAAATCGAATCGAATAC 980
Db 1 AACGCCAAACAGCCCAAGTGAACGAATTCCTCAAAAAGTCCAAATCGAATCGAATAC 60
QY 981 TACAGCTTCAACGACACAAACCTCTGGAGTAAAGGTGGAACGGGAGCTAGCTGCTGAG 1040
Db 61 TACAGCTTCAACGACACAAACCTCTGGAGTAAAGGTGGAACGGGAGCTAGCTGCTGAG 120
QY 1041 ACCAATGTACAAGACCCCAATTTTACAGGCGACGAAGAGAGAGAGGTGTGAAC 1100
Db 1041 ACCAATGTACAAGACCCCAATTTTACAGGCGACGAAGAGAGAGAGGTGTGAAC 1100

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Db	121	ACCAACTGTACAGACGCCAAATTTTACAGCGCAGGAAGAGAGAGAGAGGTGTGAACACT	180
Qy	1101	TGCTCTGGGGAGCTTCAATTTTCTACTCTGTTCCTCGGCAAGGCTTCATCGTACTTTGA	1160
Db	181	TGCTCTGGGGAGCTTCAATTTTCTACTCTGTTCCTCGGCAAGGCTTCATCGTACTTTGA	240
Qy	1161	CTGGAACACAGCATATCGCTTGTATGANGGCCATCTTATCGGTCTCTGCGTTCACCTCTGT	1220
Db	241	CTGGAACACAGCATATCGCTTGTATGANGGCCATCTTATCGGTCTCTGCGTTCACCTCTGT	300
Qy	1221	CTGTCTCGCCGCTCTTCAAGACGACATCCCGGCTCTG-CAATTTCCATTTTCTCCGGACT	1279
Db	301	CTGTCTCGCCGCTCTTCAAGACGACATCCCGGCTCTGCAATTTCCATTTTCTCCGGACT	360
Qy	1280	CATTTTCTACTTTTG 1294	
Db	361	CATTTTCTACTTTTG 375	
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LOCUS	AV190680	360 bp mRNA linear EST 22-JUL-1999	
DEFINITION	AV190680	Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite	
ACCESSION	AV190680	embryo Caenorhabditis elegans cDNA clone yk573h4 5', mRNA sequence.	
VERSION	AV190680		
KEYWORDS	EST.		
SOURCE	AV190680.1	GI:5572663	
ORGANISM	Caenorhabditis elegans.		
REFERENCE	Caenorhabditis elegans.		
AUTHORS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea		
	; Rhabditidae; Peloderinae; Caenorhabditis.		
	1 (bases 1 to 360)		
	Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,		
	Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano		
	,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and		
	Nomoto,H.		
TITLE	Expressed genes in C.elegans		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Yuji Kohara		
	Genome Biology Lab		
	National Institute of Genetics		
	Yata Iiri, Mishima, Shizuoka 411, Japan		
	Tel: 81-559-81-6854		
	Fax: 81-559-81-6855		
	Email: ykohara@lab.nig.ac.jp.		
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	/dev_stage="embryo"		
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Best Local Similarity	100.0%;	Prod. No. 1.2e-52;	
Matches 360;	Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	355	GTCTGTCTGATGACATCTCGTTCATGTGTTTCTATATAACAGTTTATAGCTTATT	414
Db	1	GTCTGTCTGATGACATCTCGTTCATGTGTTTCTATATAACAGTTTATAGCTTATT	60
Qy	415	CATGGATGGCTTATTGTACAGCTTTCTTCTTTTCTTTTCTATTCTACTACAATCTATGTG	474
Db	61	CATGGATGGCTTATTGTACAGCTTTCTTCTTTTCTTTTCTATTCTACTACAATCTATGTG	120
Qy	475	CAAGAAGTCTGAAAAGTTTCGATGTCTCCCGCGGCACATATGGTTTGGTGGACTG	534
Db	121	CAAGAAGTCTGAAAAGTTTCGATGTCTCTCCCGCGGCACATATGGTTTGGTGGACTG	180

Qy	535	GGTAACATATGGAGTTCTTCGGAATGATGTATACATTTGGAAAGTCCATTTGCGTCTGCAA	594
Db	181	GGTAACATATGGAGTTCTTCGGAATGATGTATACATTTGGAAAGTCCATTTGCGTCTGCAA	240
Qy	595	CAGTTCTACCTTATTACAAGTCTCGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCA	654
Db	241	CAGTTCTACCTTATTACAAGTCTCGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCA	300
Qy	655	GAATGGACTGTGTGGTTTGTCTGCTTTTGTATTATCTCGGTTTGGGATCTGGTTGCGGTGCTC	714
Db	301	GAATGGACTGTGTGGTTTGTCTGCTTTTGTATTATCTCGGTTTGGGATCTGGTTGCGGTGCTC	360
RESULT 6			
AV186436		360 bp	linear
LOCUS	AV186436	Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite	EST 22-JUL-1999
DEFINITION	embryo Caenorhabditis elegans cDNA clone yk499e3 5', mRNA sequence.		
ACCESSION	AV186436		
VERSION	AV186436.1	GI:5568419	
KEYWORDS	EST.		
SOURCE	Caenorhabditis elegans.		
ORGANISM	Caenorhabditis elegans		
REFERENCE	1	(bases 1 to 360)	
AUTHORS	Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.		
TITLE	Expressed genes in C.elegans		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Yuji Kohara Genome Biology Lab. National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Japan Tel: 81-559-81-6854 Fax: 81-559-81-6855 Email: ykohara@lab.nig.ac.jp.		
FEATURES	Location/Qualifiers		
source	1..360		
	/organism="Caenorhabditis elegans"		
	/strain="N2"		
	/db_xref="taxon:6239"		
	/clone="yk499e3"		
	/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"		
	/sex="hermaphrodite"		
	/dev_stage="embryo"		
BASE COUNT	103 a	62 c	85 g
ORIGIN	108 t	2 others	
Query Match	23.48;	Score 350.6;	DB 9;
Best Local Similarity	98.38;	Pred. No. 4.9e-51;	Length 360;
Matches	353;	Conservative 0;	Mismatches 6;
		Indels 0;	Gaps 0;
Qy	52	GGAGGTGCAGATCGGAAACACATACACGTTTACGGTACAAATCTGATAACAAATCGGAAT	111
Db	2	GGANGTGCAGATCGGAAACACATACACGTTTACGGTACAAATCTGATAACAAATCGGAAT	61
Qy	112	AGCCAGAAGACGAAATGTTTGGAGAAGACGGAGCTGAATACGGAGCATCTCAGCTT	171
Db	62	AGCCAGAAGACGAAATGTTTGGAGAAGACGGAGCTGAATACGGAGCATCTCAGCTT	121
Qy	172	ATTTCATCTATTGTGCGGGTGTCTACTATGCATGGCTCTGGTGTGTTTTACGATGAACACG	231
Db	122	ATTTCATCTATTGTGCGGGTGTCTACTATGCATGGCTCTGGTGTGTTTTACGATGAACACG	181
Qy	232	ATTACGTTTTTATAGTCAAAAACATGGAAAGCATTTTACTATCATCTCTTTGTCGGGAA	291
Db	182	ATTACGTTTTTATAGTCAAAAACATGGAAAGCATTTTACTATCATCTCTTTGTCGGGAA	241

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QY 292 ACAGACAGTATCGTTGAGAAGGAGTGTGATGTCACCTTGGAAAGCTCTCGTCATGTTGTGC 351
Db 242 ACAGACAGTATCGTTGAGAANGAGTGTGATGTCACCTTGGAAATGCTCTCGTCATGTTGTGC 301
QY 352 GTGGTCTGTCATGACAGTTCGCTGATGTTTCTATATAAATACAAAGTTTATAAGCT 410
Db 302 GTGGTCTGTCATGACAGTTCGCTGATGTTTCTATATAAATACAAAGTTTATAAGCT 360

RESULT 7
LOCUS AV198059 360 bp mRNA linear EST 26-JUL-1999
DEFINITION AV198059 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk674e3 5', mRNA sequence.
ACCESSION AV198059.1 GI:5581830
VERSION AV198059
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuiki, H.,
Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano
, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
Nomoto, H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="yk674e3"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 103 a 63 c 89 g 103 t 2 others
ORIGIN

Query Match 23.3%; Score 350; DB 9; Length 360;
Best Local Similarity 98.1%; Pred. No. 6.2e-51;
Matches 353; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 41 AACAGAGGCGGAGGTGCAGATCGCGAACAACATACCGTTTACGGTACAAATCTGATAA 100
Db 1 AACAGAGGCGGAGGTGCAGATCGCGAACAACATACCGTTTACNGTACAAATCTGATAA 60
QY 101 CAAATCGAATAGCCAAAGAACGAAATCTGTGGAAGACGGAGCTGAAATACGGAG 160
Db 61 CAAATCGAATAGCCAAAGAACGAAATCTGTGGAAGACGGAGCTGAAATACGGAG 120
QY 161 CATCTCACGTTATTCATCTATTTGTGCGGTGTCACTATGATCGATGGCTCTGGTTGTTTAA 220
Db 121 CATCTCACGTTATTCATCTATTTGTGCGGTGTCACTATGATCGATGGCTCTGGTTGTTTAA 180
QY 221 CGATGACACGATACGTTTATAGTCAAAACAATGGAAGGCATTTACTATCATCATCCTT 280
Db 181 CGATGACACGATACGTTTATAGTCAAAACAATGGAAGGCATTTACTATCATCATCCTT 240
QY 281 TTGTCCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGTCTACCTTGGAAATGCTCTCG 340
Db 241 TTGTCCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGTCTACCTTGGAAATGCTCTCG 300
QY 341 TCATGTTGTGCGGTGCTTCTGTATGACAGTCTCTGCTGATTTGTTTCTATAAATACAAAGT 400

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Db 301 TCATGTTGTGCGGTGCTTCTGTATGACAGTCTCTGCTGATGTTTCTATAAATACAAAGT 360

RESULT 8
LOCUS AV192017 374 bp mRNA linear EST 22-JUL-1999
DEFINITION AV192017 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk600e12 5', mRNA
sequence.
ACCESSION AV192017.1 GI:5574169
VERSION AV192017
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 374)
AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuiki, H.,
Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano
, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
Nomoto, H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
FEATURES
source
1..374
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="yk600e12"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 109 a 63 c 91 g 111 t
ORIGIN

Query Match 22.8%; Score 342.6; DB 9; Length 374;
Best Local Similarity 98.4%; Pred. No. 1.1e-49;
Matches 367; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 44 AGGAGGCGGAGGTGCAGATCGCG-AAAACACATACCGTTTACGGTACAAAATCTGATAACA 102
Db 2 AGGAGGCGGAGGTGCAGATCGCGAACAACACATACCGTTTACGGTACAAAATCTGATAACA 61
QY 103 AATCGG-AATAGCCAAGAACGAAATGTTGTGGAAGACGGAGCTGAAATACGGAGC 161
Db 62 AATCGGAATAGCCAAGAACGAAATGTTGTGGAAGACGGAGCTGAAATACGGAGC 121
QY 162 ATCTCAGTTTATTCATCTATTTGTGCGGTGTCACTATGATGCTGCTGTTGTTTTCAC 221
Db 122 ATCTCAGTTTATTCATCTATTTGTGCGGTGTCACTATGATGCTGCTGTTGTTTTCAC 181
QY 222 GATGAACACGATTACGTTTTATAGTCAAAAACATGGAAGGCATTTACTATCATCTCCTT 281
Db 182 GATGAACACGATTACGTTTTATAGTCAAAAACATGGAAGGCATTTACTATCATCTCCTT 241
QY 282 TGTCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGCTACCTTGGAAATGCTCTCGT 341
Db 242 TGTCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGCTACCTTGGAAATGCTCTCGT 301
QY 342 CATGTTGCTGCTGCTGCTGCTGATGACAGTCTCTGCTGATTTCTTCTATAAATACAAAGTT 401
Db 302 CATGTTGCTGCTGCTGCTGCTGATGACAGTCTCTGCTGATTTCTTCTATAAATACAAAGTT 361
QY 402 TTATAAGCTTTATT 414

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REFERENCE
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
        ,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
        Genome Biology Lab.
        National Institute of Genetics
        Yata 1111, Mishima, Shizuoka 411, Japan
        Tel: 81-559-81-6854
        Fax: 81-559-81-6855
        Email: ykohara@lab.nig.ac.jp.
FEATURES
source Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk216el"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 118 a 44 c 81 g 56 t 1 others
ORIGIN
Query Match 19.1%; Score 286; DB 14; Length 300;
Best Local Similarity 99.3%; Pred.No: 7.7e-40;
Matches 297; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
1114 TTCAATTTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACT 1173
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299 TTCAATTTTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACT 240
|||||
1174 ATCGCTGTGATGCGCATTCATCGTCTCTGCTTCACACAGTCTCCTGCTCGCGGTC 1233
|||||
239 ATCGCTGTGATGCGCATTCATCGTCTCTGCTTCACACAGTCTCCTGCTCGCGGTC 180
|||||
1234 TTCAACAGGACACTCCCGGCTCG-CAATTTCCATTTTCTCGGACTCATTTTTTACTTT 1292
|||||
179 TTCAACAGGACACTCCCGGCTCG-CAATTTTCCATTTTCTCGGACTCATTTTTTACTTT 120
|||||
1293 TGTACCGCTGGATCATCAACCCATTTGTACACAGTCTCACAAGTGTATTATATAT 1352
|||||
119 TGTACCGCTGGATCATCAACCCATTTGTACACAGTCTCACAAGTGTATTATATAT 60
|||||
1353 TAATTCTGTTTTTGCCATTTCTTTGCAATCAATTTTGCATATATATCTTGAGCGA 1411
|||||
59 TAATTCTGTTTTTGCCATTTCTTTGCAATCAATTTTGCATATATATCTTGAGCGA 1
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RESULT 12
C55887/c
LOCUS AV178913 300 bp mRNA linear EST 16-SEP-1997
DEFINITION C55887 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk231a7 3', mRNA sequence.
ACCESSION C55887
VERSION C55887.1 GI:2400488
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk231a7"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 116 a 44 c 81 g 56 t 3 others
ORIGIN
Query Match 19.0%; Score 285; DB 14; Length 300;
Best Local Similarity 98.7%; Pred.No: 1.2e-39;
Matches 296; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
1119 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 1178
|||||
300 TTNTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 241
|||||
1179 TTCTTATGCGCATTCATTATCGTCTCTGCTTCACCTCTGCTCGCGCTCTTCAA 1238
|||||
240 TTGTTATGCGCATTCATTATCGTCTCTGCTTCACCTCTGCTCGCGCTCTTCAA 181
|||||
1239 ACGAGCACTCCCGGCTCG-CAATTTCCATTTTCTCGGACTCATTTTTTACTTTTGTAC 1297
|||||
180 ACGAGCACTCCCGGCTCG-CAATTTTCCATTTTCTCGGACTCATTTTTTACTTTTGTAC 121
|||||
1298 CGCTCGATCATCAACCCCATTTGTTTACACAAGTCTCTCAAAAGTGTATTATTAATT 1357
|||||
120 CGCTCGATCATCAACCCCATTTGTTTACACAAGTCTCTCAAAAGTGTATTATTAATT 61
|||||
1358 CTCTGTTTGGCATTCCTTTGCATCATCAACCTTTTCGATTATATCTTGAGCGATCTCAA 1417
|||||
60 CTCTGTTTGGCATTCCTTTGCATCATCAACCTTTTCGATTATATCTTGAGCGATCTCAA 1
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RESULT 13
AV178913/c
LOCUS AV178913 300 bp mRNA linear EST 21-JUL-1999
DEFINITION AV178913 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk573h4 3', mRNA sequence.
ACCESSION AV178913
VERSION AV178913.1 GI:5558814
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="N2"
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/clone="yk573h4"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"

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Email: ykohara@lab.nig.ac.jp.
FEATURES
source Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(el489)"
/db_xref="taxon:6239"
/clone="yk231a7"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 116 a 44 c 81 g 56 t 3 others
ORIGIN
Query Match 19.0%; Score 285; DB 14; Length 300;
Best Local Similarity 98.7%; Pred.No: 1.2e-39;
Matches 296; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
1119 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 1178
|||||
300 TTNTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 241
|||||
1179 TTCTTATGCGCATTCATTATCGTCTCTGCTTCACCTCTGCTCGCGCTCTTCAA 1238
|||||
240 TTGTTATGCGCATTCATTATCGTCTCTGCTTCACCTCTGCTCGCGCTCTTCAA 181
|||||
1239 ACGAGCACTCCCGGCTCG-CAATTTCCATTTTCTCGGACTCATTTTTTACTTTTGTAC 1297
|||||
180 ACGAGCACTCCCGGCTCG-CAATTTTCCATTTTCTCGGACTCATTTTTTACTTTTGTAC 121
|||||
1298 CGCTCGATCATCAACCCCATTTGTTTACACAAGTCTCTCAAAAGTGTATTATTAATT 1357
|||||
120 CGCTCGATCATCAACCCCATTTGTTTACACAAGTCTCTCAAAAGTGTATTATTAATT 61
|||||
1358 CTCTGTTTGGCATTCCTTTGCATCATCAACCTTTTCGATTATATCTTGAGCGATCTCAA 1417
|||||
60 CTCTGTTTGGCATTCCTTTGCATCATCAACCTTTTCGATTATATCTTGAGCGATCTCAA 1
|||||
RESULT 13
AV178913/c
LOCUS AV178913 300 bp mRNA linear EST 21-JUL-1999
DEFINITION AV178913 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk573h4 3', mRNA sequence.
ACCESSION AV178913
VERSION AV178913.1 GI:5558814
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source Location/Qualifiers
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hermaphrodite embryo"

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/sex="hermaphrodite"
/dev_stage="embryo"
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Matches 29; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1118 TTCTACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACACGACTATCG 1177
DDB 300 TTTTATACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACACGACTATCG 241
QY 1178 CTGTTATGCGCATCTTATCGGCTCTGCTTCACATCTTGTCTGCTCGCGCTCTCA 1237
DDB 240 CTGTTATGCGCATCTTATCGGCTCTGCTTCACATCTTGTCTGCTCGCGCTCTCA 181
QY 1238 AAGGAGCACCCTCGGCTCTG-CAATTTCCATTTTTCGCAAGTCTCTCAAAAGTGTATTATTAAT 1296
DDB 180 AAGGAGCACCCTCGGCTCTGCAATTTTCCATTTTTCGCAAGTCTCTCAAAAGTGTATTATTAAT 121
QY 1297 CCGCTGGATCATCAACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 1356
DDB 120 CCGCTGGATCATCAACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 61
QY 1357 TCCTGTTTGGCATCTTCTTCGATCATCAACTTTTCGATTATATCTTGAGCGATCTCA 1416
DDB 60 TCCTGTTTGGCATCTTCTTCGATCATCAACTTTTCGATTATATCTTGAGCGATCTCA 1

RESULT 14
C29851/c
LOCUS
DEFINITION
C29851 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans cDNA clone yk221d3 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE
Expression map of the C.elegans genome
JOURNAL
Unpublished (1996)
COMMENT
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk221d3"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 116 a 44 c 80 g 56 t 4 others
ORIGIN
Query Match 18.7%; Score 280.8; DB 14; Length 300;
Best Local Similarity 97.7%; Pred. No. 6.1e-39;
Matches 29; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1119 TTCTACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACACGACTATCG 1178
DDB 111 TTTTATACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACACGACTATCG 1178

/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 118 a 44 c 79 g 56 t 3 others
ORIGIN
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Best Local Similarity 99.3%; Pred. No. 3.5e-38;
Matches 28; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1114 TTCATTTTACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACAGACT 1173
DDB 290 TTCATTTTACTCTGTTCTCCTCGCAAGGCTTCATCGTACTTTGACTGGAAACAGACT 231
QY 1174 ATCGCTTGTATGTGGCAATTTCTATCGTCTCTGCTTCACCTTGTCTGCTCGCGCTC 1233
DDB 230 ATCGCTTGTATGTGGCAATTTCTATCGTCTCTGCTTCACCTTGTCTGCTCGCGCTC 171
QY 1234 TTCAACAGGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCATTTTTACTTT 1292
DDB 170 TTCAACAGGACACTCCCGGCTCTGCAATTTCCATTTTCTCGGACTCATTTTTACTTT 111
QY 1293 TGTACCGCTGGATCATCAACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 1352

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Db 110 TGTACCGCTGGGATCATCCCATTTGTTACAAAGTCTCTCAAAAGTCTTTATTATAT 51
QY 1353 TAATCTCTCTTTTGGCAATTTCTTGGCATCATCAACTTTTCGATTATAT 1402
Db 50 TAATCTCTCTTTTGGCAATTTCTTGGCATCATCAACTTTTCGATTATAT 1

RESULT 16
C34382/c
LOCUS
DEFINITION
C34382 300 bp mRNA linear EST 18-OCT-1999
C34382 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans cDNA clone yk400e8 3', mRNA sequence.
C34382
ACCESSION
VERSION C34382.1 GI:2366913
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans.
REFERENCE
1 (bases 1 to 300)
; Rhabditidae; Peloderinae; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A. and Nishigaki,A.
TITLE
Expression map of the C.elegans genome
JOURNAL
COMMENT
Unpublished (1996)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
Location/Qualifiers
source
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/organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
/clone_lib="Yk400e8"
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hermaphrodite embryo"
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/dev_stage="embryo"
BASE COUNT 117 a 46 c 54 t 5 others
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Best Local Similarity 96.68; Pred. No. 1.6e-37;
Matches 286; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
QY 1108 GCGACTTCATTTCTACTGTCTCTCGCAAGGCTTCATCGTACTTTGACTGGAAC 1167
Db 296 GGGGATTCATTTNNATTTCTGTTNTCTCGCAAGGCTTCATCGTACTTTGACTGGAAC 237
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QY 1287 TACTTTTGTACCGCTGGATCATCAACCCCATTTTGTACACAAGTCTCTCAAAAGTGTTA 1346
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QY 1347 TTATATTAATCTCTGTTTTGCAATTTCTTGCATCATCAACTTTTCGATTATAT 1402
Db 56 TTATATTAATCTCTGTTTTGCAATTTCTTGCATCATCAACTTTTCGATTATAT 1

RESULT 17
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LOCUS
DEFINITION
AV175978 300 bp mRNA linear EST 21-JUL-1999
AV175978 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk400e12 3', mRNA
sequence.
AV175978
ACCESSION
VERSION AV175978.1 GI:5559859
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans.
REFERENCE
1 (bases 1 to 300)
; Rhabditidae; Peloderinae; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
TITLE
Expressed genes in C.elegans
JOURNAL
COMMENT
Unpublished (1999)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
Location/Qualifiers
source
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/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="Yk499e3"
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/sex="hermaphrodite"
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Matches 293; Conservative 0; Mismatches 4; Indels 3; Gaps 2;
QY 1114 TTCAATTTCTACTCTGTCTCTCGCAAGGCTTCATCGTACTTTGACTGGAACACGACT 1173
Db 299 TTCAATTTCTACTCTGTCTCTCGCAAGGCTTCATCGTACTTTGACTGGAACACGACT 240
QY 1174 ATCGCTTGTATGTGGCAATTTATCGGCTCTGCTTCACTCTTGTCTGCTCGCGCTC 1233
Db 239 ATCGCTTGTATGTGGCAATTTATCGGCTCTGCTTCACTCTTGTCTGCTCG-CTC 181
QY 1234 TTCAAGGAGCAGCTCCCGGCTCTGC--AATTTCCATTTTCTCGGAGCTCAATTTTACTT 1291
Db 180 TTCAAGGAGCAGCTCCCGGCTCTGCCAATTTTCCCATTTTCTCGGAGCTCAATTTTACTT 121
QY 1292 TTGTACCGCTGGATCATCAACCCCATTTTGTACACAAGTCTCTCAAAAGTGTTATATA 1351
Db 120 TTGTACCGCTGGATCATCAACCCCATTTTGTACACAAGTCTCTCAAAAGTGTTATATA 61
QY 1352 TTAATTTCTGTTTTTGGCAATTTTGGCATCATCAACTTTTCGATTATATCTTTGAGCGA 1411
Db 60 TTAATTTCTGTTTTTGGCAATTTTGGCATCATCAACTTTTCGATTATATCTTTGAGCGA 1

```

; Rhabdittidae; Peloderinae; Caenorhabdittis.

REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.

TITLE Expressed genes in C.elegans

JOURNAL Unpublished (1999)

COMMENT Contact: Yuji Kohara

Genome Biology Lab.

National Institute of Genetics

yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

FEATURES

Location/Qualifiers

1..300

/organism="Caenorhabdittis elegans"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk600e12"

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Matches 273; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 1139 GCAGGCTTCATCGTACTTTGACGTGGAACACGACTATCGTGTGTTATGTCGCAATTCTTA 1198

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QY 1199 TCGGTCTCTGCTTCACCTTTGCTGCTGCTGCTGCTTCAACAGCAGCACTCCCGGCTCG- 1257

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QY 1258 CAATTCACATTTCTCGGACTCATTTTCTACCTTTTGTACCCGCTGGATCATCACCCCAT 1317

Db 175 CAATTTCCATTTTCTCGGACTCATTTTCTACCTTTTGTACCCGCTGGATCATCACCCCAT 116

QY 1318 TTGTTACACAGTCTCTCAAGCTTTTATATATATATATATATATATATATATATATATAT 1377

Db 115 TTGTACACAGTCTCTCAAGCTTTTATATATATATATATATATATATATATATATATAT 56

QY 1378 TGCATCATCAACTTTTCGATTATATCTTGAGCGATCTCAAGCTTTTATTTACAT 1432

Db 55 TGCATCATCAACTTTTCGATTATATCTTGAGCGATCTCAAGCTTTTATTTACAT 1

RESULT 19

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DEFINITION AGENCOURT_6531717 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732941

5' mRNA sequence.

ACCESSION BM548100

VERSION BM548100.1 GI:18782416

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1101)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM12735 row: n column: 14

High quality sequence start: 9

High quality sequence stop: 643.

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1..1101

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(destroyed); Site:2: NotI; RNA source male hippocampus,

age 27. Library is oligo-df primed and directionally

cloned (EcorV site is destroyed upon cloning). Average

insert size 1.4 kb, insert size range 0.9-4 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 012."

BASE COUNT 215 a 313 c 317 g 256 t

ORIGIN

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Best Local Similarity 59.4%; Pred. No. 4.8e-29;

Matches 395; Conservative 0; Mismatches 267; Indels 3; Gaps 1;

QY 135 GGAAGAGCGGAGCTCAAAATACGAGCATCTACGTTATTATTCATCTATTTTGTGCGGTGTC 194

Db 39 GAATGAGCTGACCTCAAAATACGAGCGAAGCAGTGATCATCTGTTTGTGCTGTCAC 98

QY 195 ACTATGATGGCTCTGGTGTGTTTACGATGACACGATTACGTTTATAGTCAAAACAA 254

Db 99 TCTGTGATGATCGTGTGTTGAGTACCAATCAAGTCTGTGCGCTTCTACACAGAGAAGAA 158

QY 255 TGAAGAGCATTTACTATCATCTCTTTTGTCCGGAAACAGACAGTATCTTCAGAGGG 314

Db 159 TGGACAGC---TCATCTACACGCCATCTACTGAGGACACACCTCGTGGCCAGCGCCT 215

QY 315 ATTGATGTCACCTGGAAATGCTCTCGTCATGTTGTGGTGGTGTCTGTATGACAGTTCT 374

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QY 375 GCTGATGTTTCTTAAATACAAAGTTTATAAGCTTATTCATGGATGGCTTATTTCTCAG 434

Db 276 CTTGGTGGTCTCTACAAGTACCGCTGTACAAGTTCATCCATCGCTGGTGTGATCATGC 335

QY 435 CAGTTTCTTCTTTCTTTCTTATTTACTACTACAATCTATGTCAAGAAAGTTCTGAAAAGTTT 494

Db 336 TTCACGTGATGCTGCTCTCTCTTCACTATATCTACTTGGGGAAGTCTCAAGACCTA 395

QY 495 CGATGTGTCCTCCAGCGCACATATTGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 554

Db 396 CAATGTGGCATGGACTACCCCTCTTGTGACTGTCTGGAACCTCGGGGCACTGGG 455

QY 555 AATGATGTGTATACATTGGAAGGTCCATTGCGTCTGCAACAGTTCCTACTTATTACAT 614

Db 456 CATGTTGTGATCCACTTGGAGGGCCCTCTGTTGCTGCAGCAGCGCTACTCATCATGAT 515

QY 615 GTCTGCATTAATGGCTCTGCTCTTTTATCAAGTACCTTACCAGATGAGTGTGTGGTTGT 674

Db 516 CAGTGGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCAGAGTGTGCGCGTGGTGCAT 575

QY 675 GCTGTTTGTATCTCGTTTGGGATCTGTTGCGGTGCTCACACCAAGGACCAATGAG 734

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BASE COUNT	137 a	191 c	173 g	178 t	1 others
ORIGIN					

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Matches 384;	Conservative 0;	Mismatches 265;	Indels 3;	Gaps 1;
QY	148	CTCAAAATACGGAGCATCTCAGCTTATTCATCTATTTCGTGCGGTGTCACATGTCATGTCATGGCT	207	
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QY	208	CTGGTGTGTTTTACGATGAACACGATACGTTTTATAGTCAAAACAATGAAGGCATTGTA	267	
Db				
QY	69	GTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGC--TC	125	
QY	268	CTATCATCATCTTTTGTCCGGGAACACAGATATCGTTTGAGAGGGATGATGCATCTT	327	
Db				
QY	126	ATCTACAGCGCAATTCAGTAGGACACACCCCTCGGTGGGCCAGCGCCCTCTCAACTCCGGT	185	
QY	328	GGAAATGCTCTCGTCATGTTGTGCGTGGTGGTCTTGATGACAGTTCCTGCTGATGTTTTC	387	
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QY	186	CTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCATCTTCTTGGTGGTGCTC	245	
QY	388	TATAAATACAAGTTTTATAGCTTATTCATGGATGGCTTATTGTCACGAGTTTTCTTCCTT	447	
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QY	246	TACAAGTACCGCTGCTACAAGTTTCATCCATGGCTGGTTGATCATGCTCTTCACTGATGCTG	305	
QY	448	CTTTTCCCTATTCTACTACAACTTATGTGCAAGAAGTCTGAAAAGTTTTCGATGTGCTCCOC	507	
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QY	306	CTCTTCTCTTCCACCTATATCTACCTTGGGGAGTGCTCAAGACCTACAATGTGCCCATG	365	
QY	508	AGCGCACTATTGGTTTGTGTTGGACTGGGTAACTATGATGGAGTTCGCGAATGATGTGTATA	567	
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QY	366	GACTACCCCACTCTTGGCTGCTGAACTGTGAACTTCGGGCACTGGGTCATGTTGTCATC	425	
QY	568	CATTGGAAGAGTCCATTGCGTCTGCAACAGTTTACCTTATTACAATGTCGCACTAATG	627	
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QY	628	GCTCTGGTCTTTATCAAGTACCTACACGAATGAGACTGTGTGGTTGTGCTGTTGTTGTTATC	687	
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QY	486	GCCTTAGTGTTCATCAAGTACCTCCCAAGAGTGTCCCGTGGGTTCATCTGNGGCCCATC	545	
QY	688	TCGGTTTGGGATCTGGTTGCCGTGCTCACACAAAAGGACATTGAGATATTTCGGTGGAA	747	
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QY	546	TCTGTGTATGATCTCGTGGCTGTGCTGTGTACCATAGGGCCTCTGCAAGATGCTGGTAGAG	605	
QY	748	ACTGCACAGAGAGAAACGAGCCAAATTTTCCCGGCGCTGATTTATTCGTCTG	799	
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					Prime, mRNA sequence.				
		ACCESSION	AL553513	VERSION	AL553513.1	GI:12893418			
		KEYWORDS	EST.						
		SOURCE	'human.						
		ORGANISM	Homo sapiens						

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1006)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES	source
Location/Qualifiers	
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st.strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fullang@lifetech.com URL : http://fulllength.invitrogen.com"	
251 a	229 c 242 g 282 t 2 others
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ORIGIN	

Query Match	13.9%;	Score 207.8;	DB 9;	Length 1006;
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QY	239	TTTATAGTCAAAACATATGAAGGCATTACTATACATCTTTTGTCCGGGAACAGACA	298	
Db	454	TTTATACCCGGAGGAGTG--GCGACTAATCTATACCCCAATTCACAGAAGATTACCGAGA	510	
QY	299	GTATCGTTGAGAAGGATTTGATGTCTACTTTGGAAATGCTCTCGTCATGTTGTGCGTGGTGC	358	
Db	511	CTGTGGCCAGAGAGCCCTGCACTCAATCTGAATGCTGCCATCATGATCAGTGTCTATTG	570	
QY	359	TTCTGATGACAGTTCTGCTGATTTGTTTCTATAAATACAAGTTTTATAGCTTTATTCAATG	418	
Db	571	TTGTCATGACTATCCCTCCCTGGTGGTGTCTGTATAAATACAGGTGCTATAAGGTCATCCATG	630	
QY	419	GATGGCTTATTTGTCAGCAGCTTTCTTCTCTTTTCTCTATTCTACATAAATCTATGTGCAAG	478	
Db	631	CTGGCTTATTTATATCATCTCTATTTGCTGTGCTTTTTTTCATTCATTACTTGGGGG	690	
QY	479	AAGTTCTGAAAAGTTTCGATGTGTCTCCAGCGCACTATTGGTTTTGTTGGACTGGGTA	538	
Db	691	AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTCACCTCTGATCTGGA	750	
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Db	751	ATTTTTGGTGTGGGAATGATTTCCATTCTACTGGAAGGTCCACTTCGACTCCGACAGG	810	
QY	599	TCTACCTTATTACAATGCTCGCAATAATGGCTCTGTGCTTTTATCAAGTACCTACCAGAAT	658	
Db	811	CATATCTCATTATGATTAGTGCCCTCATGGCCCTGTGTATTATCAAGTACCTCCCTGGAAT	870	
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3-CT0219-280100-062-111&t3=2000-01-28&t4=1)
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 High quality sequence stop: 639.

FEATURES

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 /note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 180 a 149 c 166 g 218 t 1 others
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 Matches 331; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
 QY 253 AATGGAAGGCATTACTATCACATCCCTTTTGTCCGGAAACACACAGTATCGTTGAGAAG 312
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 QY 373 CTGCTGATGTTCTTCTAATAACAAGTTTATAAGCTTATTATGATGGCTTATTGTC 432
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 DB 391 ATTAGTCCCTCATGCGCCCTGGTGTATTATCAAGTACCTCCCTGAATGACTGCGTGC 450
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 DB 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTAC 570
 QY 793 TCCTC 797
 DB 571 TCCTC 575

RESULT 32
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 DEFINITION IL3-CT0219-160200-063-C04 CT0219 Homo sapiens cDNA, mRNA sequence.
 AW850636
 ACCESSION
 VERSION AW850636.1 GI:7946153

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 735)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3-CT0219-160200-063-C04&t3=2000-02-16&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 728.

FEATURES

source
 1. 735
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 188 a 152 c 176 g 218 t 1 others
 ORIGIN
 Query Match 13.5%; Score 202.6; DB 10; Length 735;
 Best Local Similarity 60.7%; Pred. No. 1.2e-25;
 Matches 331; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
 QY 253 AATGGAAGGCATTACTATCACATCCCTTTTGTCCGGAAACACACAGTATCGTTGAGAAG 312
 DB 31 AAGGATGGCGAGCTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCACAGA 90
 QY 313 GGATTTGATGTCATTGGAAATGCTCTCGTCATGTTGGCGTGTGCTGTTCTGTGATGACAGTT 372
 DB 91 GCCTGTCACCTCAATTCCTGAATGCTGCCATCATGATGATGCTGTTGTCATGACTATC 150
 QY 373 CTGCTGATGTTCTTCTAATAACAAGTTTATAAGCTTATTATGATGGCTTATTGTC 432
 DB 151 CTCCTGTGGTCTGTATAAATACAGTGTCTATAAGGTCAATCCATGCTGCTTATTATA 210
 QY 433 AGCAGTTTCTTCTCTTTTCCCTATTACACTACATCTATGTGCAAGAAGTCTTCAAAAGT 492
 DB 211 TCATCTCTATTGTTGCTGTTCTTTTTCATTCTATTACTTGGGGAAGTGTAAAC 270
 QY 493 TTCGATGTGTCCTCCAGCGCATTATGTTTGTGGACTGGGTGAACACTATGAGGTTCTC 552
 DB 271 TATAACGTTGCTGTGGACTACATCTACTGTTGSCACTCTGATCTGGAATTTTGGTGGTG 330
 QY 553 GGAATGATGTATACATTGGAAGGTCCATTGGCTCTGCAACAGCTTCTACCTTATTACA 612
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[illegible]

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LOCUS	AWS50727
DEFINITION	IL3-CT0219-160200-064-H05 CT0219 Homo sapiens cDNA, mRNA linear EST 19-MAY-2000
ACCESSION	AWS50727
VERSION	AWS50727.1 GI:7946244
KEYWORDS	EST.
SOURCE	human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 573)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M. R., Nagai, M. A. da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A. J., deOliveira, P. S., Bucher, P., Jongseneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=I13-CT0219-160>)
200-064-H058t3-2000-02-16t54-1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 481.

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FEATURES
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        /dev_stage="Adult"
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        from ORESTES PCR (U.S. Letters Patent application No. 196
        716 - Ludwig Institute for Cancer Research) profiles
        into the pUC 18 vector. Reverse transcription of tissue
        mRNA and cDNA amplification were performed under low
        stringency conditions."

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Best Local Similarity	60.7%; Pred. No. 1.6e-25;			

Query Match 13.5%; Score 202.2; DB 10; Length 573;
Best Local Similarity 60.7%; Pred. No. 1.6e-25;

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QY	283	GTCGGGAACACACAGCATATCGTTTGAGAGGGGATTGATGTCTACTTGGAAATGCTCTCGTC	342						
Db	59	ACAGAAGATACCGAGACTGTGGCCAGAGAGCCCTGCACCTAATTCGTAATGCTGCCATC	118						
QY	343	ATGTTGTCGTGGTTCCTGATGACAGTTCCTGCTCATTTGTTTTCTATATAACACAAGTTT	402						
Db	119	ATGATCAGTGTCAATGTTGTCAAGCACTATCCTCCTGGTGTCTGTATAAATACAGGTGC	178						
QY	403	TATAAGCTATTTCATGGATGGCTATTGTGCAGCAGTTTTCTTCTTTTCCCTATTTCAC	462						
Db	179	TATAAGTTCATCCATGCCTGGCTATTATATCATCTCTATTGTGCTGTCTTTTTTCA	238						
QY	463	ACAATCTATGTCAAGAAGTCTGAAAGATTTCGGATGTCTCCCGACGGCAGCATATTGGTT	522						
Db	239	TTCATTTCATTGGGGGAAGTGTTTAAAGCTATAAGCTTGCTGTGGACTACATACTGTT	298						
QY	523	TTGTTTGGACTGGGTAACTATGGAGTTCCTCGGAATGATGTGTATACATTGGAAAGTCCA	582						
Db	299	GCACCTCTGATCTGGAAATTTGGTGTGGTGGGAATGATTTCCATCTACCTGGAAAGGTCCA	358						
QY	583	TTGCGTGTCAACAGTTCTACCTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATC	642						
Db	359	CTTCGACTCCACAGGCATATCTCAATTATGATTAGTGCCCTCATGGCCTGGTGTATC	418						
QY	643	AAGTACCTACCAGAAATGGACTGTGGTGTGTGCTGTTTGTGTTATCTCCGGTTGGGATCG	702						
Db	419	AAGTACCTCCCTCAATGGACTGGTGGCTCACTCTTGGCTGTGATTTTCAGTATATGATTTA	478						
QY	703	GTTCGCGTGTCTACACCAAAAGACCATTTGATGATATTTGGTGGAACTGCACAGGAGAGA	762						
Db	479	GTGCTGGTTGTGTCGGAAGGTCCACTTCGTATGCTGGTGTGAACAGCTCAGGAGAGA	538						
QY	763	AACAGCCCAATTTTCCCGGGGTGATTTATTCGT	797						
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RESULT	34
LOCUS	AW604307
DEFINITION	IL13-CT0219-280100-062-D09 CT0219 Homo sapiens cdna, mRNA linear
ACCESSION	AW604307
VERSION	AW604307.1 GI:7309048
	EST 23-MAR-2000 mRNA sequence.

SOURCE: human.
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 601)
HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE: The FAPESP/LICR Human Cancer Genome Project
JOURNAL: Unpublished (1999)
COMMENT: Contact: Simpson A. J. G.

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL3&t4=1>)
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 Seq primer: puc 18 forward
 High quality sequence stop: 600.
 Location/Qualifiers:

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/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 138 a 128 c 135 g 199 t 1 others
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Best Local Similarity 60.6%; Pred. No. 2e-25;
Matches 330; Conservative 0; Mismatches 215; Indels 0; Gaps 0;
QY 253 AAGTGAAGGCAATTTACTATACATCCCTTTTGTCCGGGAACAGACAGATATCGTTGAGAAG 312
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QY 313 GGATTCATGTCATCTGGAATGCTTCGCATGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 372
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91 GCCTGCACCTCAATTCGATGCTGCCATCATGATCAGTGTGCTATGTTGTGTCATGACTATC 150
QY 373 CTGCTGATGTTCTTCTATATAAACAAGTTTATAAGCTTATTCATGATGCTTATTTGTC 432
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151 CTCTGTGTGTTCTGTATAAATACAGGTGCTAATAGTCAATCCATGCTGCTGCTTATATA 210
QY 433 AGCAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 492
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211 TCATCTCTATGTTGCTGTTCTTTTTCATTTACTTTGTTGGGGAAGTGTAAACC 270
QY 493 TTCGATGTGTCCTCCAGGCACATATGTTGTTGTTGGACTGGGTACTATGAGTTCCT 552
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 TATAAGCTGTGCTGGCACTACATCTACTGTTGCACCTCTGATCTGGAATTTGTTGTGGTG 330
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391 ATTAGTCCCTCATGCGCCCTGTTTATCAAGTACCTCCTGAATGCACTGCGTGGCTC 450
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451 ATCTTGCTGCTGATTTTCAGTATATGATTTAGTGGCTGTTTGTGTCGGAAGGTCCACTT 510
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Db ||| |||
571 TCCTC 575

RESULT 35
AW850572
LOCUS
DEFINITION IL3-CT0219-160200-060-H02 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW850572
VERSION AW850572.1 GI:7946089
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 757)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
```

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TITLE
JOURNAL
MEDLINE
COMMENT
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-il3-ct0219-160
200-060-H02&t3=2000-02-16&t4=1)
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High quality sequence start: 5
High quality sequence stop: 755.
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/clone_lib="CT0219"
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 193 a 159 c 181 g 223 t 1 others
ORIGIN
Query Match 13.4%; Score 201.6; DB 10; Length 757;
Best Local Similarity 59.6%; Pred. No. 1.8e-25;
Matches 358; Conservative 0; Mismatches 240; Indels 3; Gaps 1;
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2 TATCCCCGAAACATGCCGTGCTACCATTAAGTCAGTCAGCTTTTATACCGGAAGATG 61
QY 257 GAAGGCATTTACTATACATCCCTTTTGTCCGGGAACAGACAGATATCGTTGAGAAGGAT 316
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
62 ---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCAGAGAGCC 118
QY 317 TGATGTCACATGGAAATGCTCTCGTCATGTTGTGCGTGGTCTCTCATGACATTTCTGC 376
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
119 TGCACCTCAATCTGAATGCTGCCATCATGATCATGTCATGTTGTCTGATGACTATCTCC 178
QY 377 TGATTTGTTTCTATAAATAACAAGTTTATAGCTTATTCATGATGATTTATTTCTCAGCA 436
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 TGGTGGTCTGTATAAATACAGGTGCTATAGGTCATCCATCGCTTATATATCAT 238
QY 437 GTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 496
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
239 CTCTATTTGTTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 298
QY 497 ATGTGTCCTCCAGGCACATATGTTTGTGACTGGGTAACTATGAGATTTCTCGGAA 556
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 557 TGATGTCATATACATTTGAAAGGTCATTTGGCTCTCGAACAGCTTCTACCTTATTAACAATG 616
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LOCUS IL3-CT0219-160200-060-H03 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW850573
ACCESSION AW850573
VERSION AW850573.1 GI:7946090
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT

Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-IL3-CT0219-160

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High quality sequence stop: 532.

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/note="Organ: colon; Vector: puc18; Site:1; Sma1; Site:2;
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from ORESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 135 a 130 c 130 g 197 t 1 others

ORIGIN

Query Match

Best Local Similarity 13.4%; Score 201.4; DB 10; Length 593;

Matches 350; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

FEATURES

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source

1..599

source

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Db 126 CATCATGATCAGTGTCAATGTTGTGATGACTATCCCTCTGCTGCTGATATAACAG 185
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Qy 459 CACTACAACTATGTCGAAGAAGTTCGAAAAGTTTCGATGTCGTCTCTCCAGCGCACTATT 518
Db 246 TTCAATCATTTACTTGGGGGAAGTGTAAACCTATAACGTTGCTCTGGACTACATFAC 305
Qy 519 GGTGTTTGTGGTGGTAACTATGAGTTCCTCGGAATGATGTGTATACATTTGGAAGG 578
Db 306 TGTGCACTCTGATCTGGAATTTGGTGTGGTGGGAATGATTTCCATTCACCTGGAAGG 365
Qy 579 TCCATTCGCTCGACAGATTTCTACCTTATACAAAGTCTGCACCTAATGGCTCTGGTCT 638
Db 366 TCCACTTCGACTCCAGCAGCATATCTCATTATGATTAGTGGCTCATGSCCTCATGSCC 425
Qy 639 TATCAAGTACTACCAAGATGAGCTGTGTGTTTGTGCTCTTTGTTATCTCCTGTTTGGGA 698
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Qy 759 GAGAAAGACGCAATTTTCCGGCGCTGATTTATTCGTC 797
Db 546 GAGAAATGAACGCTTTTCCAGCTCTCATTTACTCTC 584

RESULT 37
AW604231

LOCUS

DEFINITION

IL3-CT0219-210100-059-C05 CT0219 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW604231

VERSION AW604231.1

KEYWORDS GI:7308972

SOURCE EST.

ORGANISM human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 599)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-

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High quality sequence stop: 563.

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source

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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 137 a 128 c 134 g 199 t 1 others
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Query Match 13.4%; Score 201.4; DB 10; Length 599;
Best Local Similarity 60.9%; Pred. No. 2.2e-25;
Matches 328; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
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Qy 31 AAGGATGGCAGCTAATCTATACCCATTCACAGAAGATACCGAGACTGTGGCCAGAGA 90
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 313 GGATTGATGTCACATGGAAATGCTCTGTCATGTTGCGTGGTCTGTTCTCATCAGAGT 372
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 373 CTGCTGATTTCTTCTATAAACAAGCTTTTATAAGCTTTTATCATGGATGGCTTATGTC 432
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Qy 151 CTCCTGGTGTCTGTATAAATACAGGTGCTATAAGGTCCATCCGCTGGCTTATATA 210
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Qy 433 AGCAGTTTCTCTCTCTTTTCCATTCACACATCATGTCGAAGAAGTCTGAAAGT 492
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Qy 211 TCATCTCTATTTGCTGTCTCTTTTTCATCTTACTTGGGGAAGTGTATAAAC 270
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Qy 271 TATACCTGTCTGGGACTACATTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 553 GGAATGATGATATACATTTGGAAGGTCATTTGCGTCTGCAACAGTTCTACCTATTACA 612
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 331 GGAATGATTTCCATTCCTGAAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 613 ATGCTCGCATATGCTCTGCTTTTATCAAGTACCTACAGATGCTGCTGCTGCTGCTG 672
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 391 ATTAGTCCCTCATGCGCCCTGGTGTATCAAGTACCTCCCTGAAAGTGGCTGCTGCTC 450
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 673 GTGCTGTTGTTATCTCGGTTTGGGATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 451 ATCTTGCTGTGATTTTCAATATATGATCTAGTGTGCTGTTTGTGTCGAAAGTCCACT 510
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 733 AGATATTTTGTGGAAGTGCAGAGAGAGAAACAGGCAATTTTCCGCGGCTGATTTA 791
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Qy 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTA 569
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 38
AW850632/c
LOCUS
DEFINITION IL3-CT0219-160200-063-B04 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW850632
VERSION AW850632.1 GI:7946149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 737)
REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
```

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sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et3-IL3-CT0219-160
200-063-B04&t3=2000-02-16&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 715.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 218 a 178 c 152 g 187 t 2 others
ORIGIN
Query Match 13.4%; Score 200.4; DB 10; Length 737;
Best Local Similarity 60.6%; Pred. No. 3e-25;
Matches 327; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
Qy 258 AAGGCTTTTACTATACATCTCTTTTGTCCGGAAACACAGATATCGTTGAGAAGGATT 317
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Qy 318 GATGCTCACTTGGAAATGCTCTCGTCATGTTGTGGTGGTGGTGGTGGTGGTGGTGGT 377
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 677 GCATCAATTTCTGAATGCTGCCATCATGATCATGATGATGATGATGATGATGATGAT 618
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Qy 378 GATTGTTTCTTATAAATACAGTTTATAAGCTTATCATGATGGTCTTATTGTCAGCAG 437
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 498 TGTCTCTCCAGCCACTATTTGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 557
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 497 CGTTGCTGTGGACTACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 558 GATGCTATACATTTGGAAGTCCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 437 GATTTCATTCCTGGAAGGTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 618 TGCATAATGGCTCTGGTCTTTTATCAAGTACCTACCAGAATGGACTGTGTGTGTGTGT 677
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 377 TGCCTCATGCGCCCTGGTGTATTATCAAGTACCTCCCTGAAATGGAGTGGTGGTCACT 318
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Qy 678 GTTTGTATTCGGTGTGGGATCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 737
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Qy 317 GGCTGATTTTCAGTATATGATTTAGTGGCTGTTTGTGTCGGAAGGTCACCTTCGAT 258
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 738 TTTGGTGAAGTGCACAGGAGAGAAAGCCCAATTTTCCCGGCTGATTATTTCGTC 797
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Qy 257 GCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTCAGCTCCTCACTTACTC 198
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RESULT 39
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DEFINITION    IL3-CT0219-160200-064-C06 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION     AW850712
VERSION       AW850712.1 GI:7946229
KEYWORDS      EST.
SOURCE        Homo sapiens
ORGANISM      human.
REFERENCE     Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
AUTHORS       Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
              M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE       20202663
COMMENT       Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=IL3-CT0219-160
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              Seq primer: puc 18 forward
              High quality sequence stop: 560.
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                  /dev_stage="Adult"
                  /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                  SmaI; A mini-library was made by cloning products derived
                  from ORESTES PCR (U.S. Letters patent application No. 196
                  ,716 - Ludwig Institute for Cancer Research) profiles
                  into the puc 18 vector. Reverse transcription of tissue
                  mRNA and cDNA amplification were performed under low
                  stringency conditions."
BASE COUNT    135 a 128 c 126 g 192 t
ORIGIN
Query Match      13.3%; Score 200; DB 10; Length 581;
Best Local Similarity 60.5%; Pred. No. 3.9e-25;
Matches 329; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 253 AATGGAAGGCATTACTATACATCCTTTTGTCCGGGAACAGACAGATATCGTTGAGAAG 312
Db 31 AAGGATGGGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCACAGAGA 90

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Db 91 GCCTGCATCAATCTGGAATGCTGCCATCATCATGATCATGTCATTGTGTCATGACTATC 150

QY 373 CTGCTGATTTCTTTATATAAATAAGTTTATTAAGCTTATTCATGATGATGCTTATTGTC 432
Db 151 CTCTGGTGGTTCGTATATAATACAGGTGCTATAGGTATCATCCATCGCTGGCTTATATA 210

QY 433 AGCAGTTTCTCTCTTTCCCTATTACATACATATATGTCGAAGAAGTCTGAAAGT 492
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QY 493 TTCGATGTCCTCCAGCGCACTATTGGTTTGTGTTGGACTGGGTAACTATGAGTTC 552
Db 271 TATAAGTTGCTGTGGACTACATTTACTTGTGCACTCCTGATCTGGAATTTTGTGTGGTG 330

QY 553 GGAATGATGTTATACATTTGGAAGTCCATTCGCTCTGCAACAGTTCCTACCTTATTACA 612
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QY 613 ATGTCCTGCACTAATGCTCTGTGTTTATCAAGTACCTACCAAGATGGAGTGTGGTTT 672
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QY 673 GTGCTGTTGTTATCTCGGTTTGGGATCTGGTTCGCTGCACACAAAGACCAATG 732
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QY 733 ACATATTTGCTGGAACACTCCAGAGAGAGAAAGCCCAATTTCCCGCGCTGATTTAT 792
Db 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAACGCTTTTCCAGCTCTCATTTAC 570

QY 793 TCCT 796
Db 571 TCCT 574

RESULT 40
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LOCUS         IL3-CT0219-271099-022-C05 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION    AW376912
ACCESSION     AW376912
VERSION       AW376912.1 GI:6881575
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         HCGP http://www.ludwig.org.br/ORESTES.
JOURNAL       The FAPESP/LICR Human Cancer Genome Project
COMMENT       Unpublished (1999)
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-CT0219-
              271099-022-C05&t3=1999-10-27&t4=1)
              Seq primer: puc 18 forward
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                  /dev_stage="Adult"
                  /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
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                  from ORESTES PCR (U.S. Letters patent application No. 196
                  ,716 - Ludwig Institute for Cancer Research) profiles
                  into the puc 18 vector. Reverse transcription of tissue
                  mRNA and cDNA amplification were performed under low
                  stringency conditions."
BASE COUNT    135 a 127 c 126 g 197 t
ORIGIN
Query Match      13.3%; Score 200; DB 10; Length 585;
Best Local Similarity 60.5%; Pred. No. 3.9e-25;

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QY	313	GGATTGATGC	ACTTGGAAATGCT	CTCGTCATGTTGTGCGTGGTCTGATGACAGATT	372					
Db	104	GCCTGCAC	TCAATCTGTAATGCT	GCCATCATGATCAGTGTCAATGTTGTTCATGACATC	163					
QY	373	CTGCTGATTC	TTTCTATATAATACA	AGCTTTTATAAGCTTATTCATGATGCGTATTATGTC	432					
Db	164	CTCCTGGT	GTCTGTATAAATCAG	GTGCTATAAGTCAATCCATGCTGGCTTATTATATA	223					
QY	433	AGCAGTTTT	CTTCTTTCTTTTCT	TATTCACATACATCTATGCAAGAAGTTCTGAAAAGT	492					
Db	224	TCATCTCT	ATTGTTGCTGTCTTT	TTTTCATTCATTTACTTTGGGGAAAGTCTTTAAACC	283					
QY	493	TTGATGTG	TCTCCAGCGCACTA	TATGGTTTTGTTGGACTGGGTACTATGAGATTCTC	552					
Db	284	TATAAGCT	TGCTGTGGACTACAT	TACTGTTTGGACTCTGATCTGGAATTTTGGTGTGGT	343					
QY	553	GGAAATGAT	GTATACATTGGAAG	PGCCATTCGCTCGCAACAGTCTACCTTATTATACA	612					
Db	344	GGAAATGAT	TTCATCTACTGGA	AAAGTCCACTTCGACTCCAGCAGGCATATCTCATTTATG	403					
QY	613	ATGCTGCACT	AAATGGCTCTGGTCT	TATCAAAGTACCTACAGAATGGACTGTGTGTTTT	672					
Db	404	ATTAGTGC	CCCTCATGGCCCTGG	TGTTTATCAAGTACCTCCCTGAAATGGACTGCGTGCTC	463					
QY	673	GTGCTGTT	GTGTTATCTCGGTT	TGGGATCTGGTTCGCGTGTCTCACACAAAGGACCAATTG	732					
Db	464	ATCTTGGCT	GTGATTTTCAGTAT	ATGATTTAGTGGCTGTTTGTGTCCAAAAGGTGCCACTT	523					
QY	733	AGATATT	TGTTGGAAACTGC	CACAGGAGAGAAACGAGCCAATTTTCCCGCGCTCATATTAT	792					
Db	524	CGTATC	TGCTGTTGAAACAG	CTCATGAGAGAAATGACACGCTTTTTCACATCTCATTTTAC	583					
QY	793	TC	794							
Db	584	TC	585							

RESULT	41
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ACCESSION	AW604313
VERSION	AW604313.1
KEYWORDS	EST; GI:7309054
SOURCE	human
SOURCE	

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 592)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A. J. G.

Contact: Simpson A.R.O.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3st2-IL3-CT0219-280100-062-F11st3-2000-01-28st4+1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 589.
 Location/Qualifiers

FEATURES

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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
134 a 1328 c 132 g 197 t 1 others
BASE COUNT

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ORIGIN					
Query Match	13.3%	Score 200;	DB 10;	Length 592;	
Best Local Similarity	60.4%;	Pred. No. 3.9e-25;			
Matches 329;	Conservative 0;	Mismatches 216;	Indels 0;	Gaps 0;	
Qy	253	AATGGAAGGCATTTACTATACACATCCCTTTTTCGCGGAAACAGACAGATATCGTTGTGAGAG	312		
Db	31	AAGGATGGCAGCTAATCTATACCCCATACAGAAGATACCGAGACTGTGGCCACAGA	90		
Qy	313	GGATTGATGTCACCTTGGAAATGCTCTCGTCATGTTGTCGGTGGTCGTTCTGATGACACGTT	372		
Db	91	GCCTGCACTCAATCTTGAATGCTGCCATCATGATCAGTGTCAATGTTGTGCATGACTATC	150		
Qy	373	CTCGTATGTTTCTTAATAACAAGCTTTTATAAGCTTATTCAAGTATTCATGATGGCTTATTGTC	432		
Db	151	CTCCTGGTGTCTGTATAATACAGGTGCTTTAAGGTCATCCATGCTGGCTTATTATA	210		
Qy	433	AGCAGTTTTCTCTCTTTTCCCTATTCACTACAACTATGTGCAAGAAGTTCTGAAAAGT	492		
Db	211	TCATCTCTATTGTGTGTTCTTTTTTTCATTTCATTTACTTGGGGAAAGTGTTTAAACC	270		
Qy	493	TTCGATGTGTCCTCCACGGCACTATTGGTTTTGTTTGGACTGGGTGAACATATGGAGTCTC	552		
Db	271	TATAACGTTGCTGTGGACTACATTACTGTTGTCACCTCTGATCTCGGAATTTTGGTGTGGTG	330		
Qy	553	GGATGATGTGTATACATTTGGAAAGGCCAATTCGCTGTGCAACAGTTCTACCTTATTACA	612		
Db	331	GGATGATTTCCATTCAGTGAAGSTCCACTTCGACTCCAGCAGGCATATCTCATTTAG	390		
Qy	613	ATGTCGCACTAATGGCTCTGGTCTTTATCAAGTACCTACAGAAATGGAGCTGTGTGGTTT	672		
Db	391	ATTAGTCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTC	450		
Qy	673	GTGCTGTTTGTATCTCGGTTTGGATCTGGTTGCCGTGCTCACACCAAAAGGACCATTG	732		
Db	451	ATCTTGCTGTGATTTTCAGTATATGATTTAGTGTGCTGTTTGTGTCCGAAAGGTCACCTT	510		
Qy	733	AGATATTTTGGTGGAAACTGGACAGGAGAAACGAGCAATTTTCCCGCGCTCATTTTAT	792		
Db	511	CGATGCTGTTGAAACAGCTCANGAGAGAAATGAACGCTTTTTCAGGCTCTCATTTAC	570		
Qy	793	TCGTC 797			
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RESULT	42
LOCUS	AW850561
DEFINITION	IL3-CT0219-160200-060-A06 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW850561
VERSION	AW850561.1 GI:7946078
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 591)
AUTHORS	Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R.,

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st3-IL3-Cr0219-160
200-063-D10st3-2000-02-16st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 569.
Location/Qualifiers
1. 570
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/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
, 716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 131 a 123 c 126 g 190 t

ORIGIN

Query Match 13.2%; Score 198.2; DB 10; Length 570;
Best Local Similarity 60.5%; Pred. No. 8.1e-25;
Matches 326; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 253 AATGGAAGGCATTTACTATACATCCCTTTTGTCCGGGAACAGACAGTATCGTTGAGAAG 312
DB 31 AAGCATGGCAGCTAACTATACCCCATTCACAGAAGATCCGAGAGCTGGGGCCAGAGA 90
QY 313 GGATTGATGCACCTTGAATGCTCTCGTATGTTTGGTGGTGGTCTTGTATGACAGATT 372
DB 91 GCCCTGCACCTAATTCGAATGCTGCCATCATGATCATGATGTCATGTTGTGATGACTATC 150
QY 373 CTGCTGATTTCTTCTATAAACAAGTTTATPAAGCTTATTCATGATGCTTATTTGTC 432
DB 151 CTCCTGGTGGTCTGTATTAATACAGTGTCTATPAAGTCTATCCATGCTGCTTATTTATA 210
QY 433 AGCAGTTTTCTTCTTTCTTCTATTCACATCAATCTATGTGCAAGAGTTCTGAAAAGT 492
DB 211 TCATCTCTATTGTTGCTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 270
QY 493 TTCATGTTGCTCCAGCGGCACTATGTTTGTGTCATGTTGCTGATGTTGCTGATGTTGCTC 552
DB 271 TATAACGTTGCTGTGGACTACATCTACTGTTGCACTCTCTGATCTGGAATTTTGTGTGGT 330
QY 553 GGAATGATGCTATACATGGAAGGTCCTATGCTGCTGCAACAGTTCTACCTTTATTACA 612
DB 331 GGAATGATTTCCATCTACTGGAAGGTCCTATGCTGCTGCAACAGTTCTACCTTTATTACA 390
QY 613 ATGCTGCACCTAATGGCTCTGGTCTTTATCAAGTACCTACCAAGTGGTGTGTTT 672
DB 391 ATTAGTGCCTCATGGCCCTGGTGTATCAAGTACCTCCCTGAATGGCTGCGTGC 450
QY 673 GTGCTGTTTGTATCTCGTTTGGGATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
DB 451 ATCTTGGCTGTTGTTTCAAGTATATGATTTAGTGGCTGTTTGTGCTGCTGCTGCTGCTGCT 510
QY 733 AGATATTTGGTGAAGTGCACAGAGAGAAACAGGCAATTTTCCCGGCGCTCATTTA 791
DB 511 CGTATGCTGGTGAACAGCTTAGAGAGAAATGAACGCTTTTCCAGCTCTCATTTA 569

RESULT 46
AW850639
LOCUS

DEFINITION IL3-CT0219-160200-063-D11 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW850639
VERSION AW850639.1 GI:7946156
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 614)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT

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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st3-IL3-Cr0219-160
200-063-D11st3-2000-02-16st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 486.
Location/Qualifiers
1. 614
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/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"

FEATURES
source

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
, 716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 146 a 133 c 141 g 194 t
ORIGIN

Query Match 13.2%; Score 197.8; DB 10; Length 614;
Best Local Similarity 60.2%; Pred. No. 9.2e-25;
Matches 328; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 253 AATGGAAGGCATTTACTATACATCCCTTTTGTCCGGGAACAGACAGTATCGTTGAGAAG 312
DB 31 AAGCATGGCAGCTAATCTATACCCCATTCACAGAAGATCCGAGACTGGGGCCAGAGA 90
QY 313 GGATTGATGCACCTTGAATGCTCTCGTATGTTTGGTGGTGGTCTTGTATGACAGATT 372
DB 91 GCCCTGCACCTAATTCGAATGCTGCCATCATGATCATGATGTTGTGATGACTATC 150
QY 373 CTGCTGATTTTCTTCTATAAACAAGTTTATPAAGCTTATTCATGATGCTTATTTGTC 432
DB 151 CTCCTGGTGGTCTGTATAAATACAGTGTCTATPAAGTCTATCCATGCTGCTTATTTATA 210
QY 433 AGCAGTTTTCTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 492
DB 211 TCATCTCTATTGTTGCTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 270

FEATURES source Location/Qualifiers
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/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
137 a 128 c 135 g 200 t 1 others

BASE COUNT 137 a 128 c 135 g 200 t 1 others
ORIGIN
Query Match 12.8%; Score 191.6; DB 10; Length 601;
Best Local Similarity 60.48; Pred. No. 1.1e-23;
Matches 350; Conservative 0; Mismatches 225; Indels 4; Gaps 2;
QY 220 ACCGATGAACACGATTTAGCTTTTATAGTCAAAACAATGGAAGGATTTACTATCACATCCCT 279
DB 1 ACCATTAAAGTCGTCAGCTTTTATACCGGAAGATG--GGCAGCTAACTATACCCCA 57
QY 280 TTGTCCGGGAACACAGACATATCGTTGAGAGGATGTATGTCACATTGGAATGCTCTC 339
DB 58 TTCACAGAATACCGAGACTGTGGGCACAGAGCCCTGCACCTCAATTTCTGAATGCTGCC 117
QY 340 GTCATGTGTGCTGGTGTCTGATGACAGTTCTGCTGATTTCTTCTATAATACAAG 399
DB 118 ATCATGATCAGTGTGATGTCAGCATATCCTCTGTGTGCTCTGTATAATACAGG 177
QY 400 TTTTATAAGCTTATTCATGATGGCTTATTTGTCAGCAGTCTTTCTCTCTTTTC-CTATT 458
DB 178 TGCTATAAGCTCATCGCTGGCTTATTATATATCATCTCTATTGTTGCTGTTCTTTT 237
QY 459 CACTACAACTATGTGCAAGAAGTCTGAAAAGTTTCGATGTCTCTCCAGCGCACTATT 518
DB 238 TTCATTCTTACTTGGGGAAGTGTATAAAGCTATAAGCTTGTGCTGTGACATACATTAC 297
QY 519 GGTTTTGTGGACTGGGTAACTATGAGTTCGGAATGATGTGTATACATTGGAAGG 578
DB 298 TGTGCACTCCTGATCTGGAATTTTGTGTGGGGAAGATTTCCATTCACTTGGAAAGG 357
QY 579 TCCATTGCGTCTGCAACAGTCTACCTTATTAACATGTCGCACTAATGCTCTGCTCTT 638
DB 358 TCCACTTCGACTCCAGCAGCATATCTCATATGATTAGTGCCTCATGSCCCTGGTGT 417
QY 639 TATCAAGTACTACCAGAAATGGAGTGTGCTGTGCTGTGCTGTTGTTATCTCGGTTGGGA 698
DB 418 TATCAAGTACTCCCTGAATGGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 477
QY 699 TCTGTTGTCGCTGCTACACAAAGACCAATGAGATATTGTTGGTGAAGACTGCACAGGA 758
DB 478 TTTAGTGGCTGTTTGTGTCGGAAGGTCCACTTCGATGCTGTGTTGAAACAGCTCANGA 537
QY 759 GAGAAAGACGCCAATTTTCCCGCGCTGATTTATTTCGT 797
DB 538 GAGAAATGAACAGCTTTTCCAGCTCTCTATTACTCTC 576

RESULT 49
AW367487
LOCUS
DEFINITION
MR0-HT0164-141199-009-h05 HT0164 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW367487
VERSION
AW367487.1 GI:6872137
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 590)

AUTHORS
TITLE
JOURNAL
COMMENT

HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES

source

1.590

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0164"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

133 a 130 c 140 g 187 t

BASE COUNT

ORIGIN

Query Match 12.7%; Score 190.4; DB 10; Length 590;
Best Local Similarity 60.08; Pred. No. 1.8e-23;
Matches 317; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 253 AATGGAAGGATTTACTATCACATCCTTTTGTCCGGAAACAGACAGTATCGTTGAGAAG 312

DB 36 AAGGGTGGCAGCTAATATATACCCCATTCACAGAAGATACCGAGACTGTGGCCAGAGA 95

QY 313 GGAATGATGTCATTTGGAATGCTCTCGTCATGTTGTGCGTGTGCTGTTGATGACAGATT 372

DB 96 GCCTCGACTCAATCTGAATGCTGCGCATCATGATCAGTGTGTTGTCATGACTATC 155

QY 373 CTGCTGATTTTCTATTAATAACAAGTTTATAAGCTTATTCATGATGGCTTATTGTC 432

DB 156 CTCTGGTGTCTGTATTAATAACAGGTGCTTAAGGTCATCCATCGCTGGCTTATTATA 215

QY 433 AGCAGTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 492

DB 216 TCATCTCTATTTGGGCTGTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 275

QY 493 TTGATGTCCTCCAGCGCACTATTGGTTTCTTGGAGTGGGTAACTATGAGTTCCTC 552

DB 276 TATAAGCTTGTCTGTGGACTACATTTACTTGTGCTACTCTGCTGGAATTTGGGGGTGG 335

QY 553 GGAATGATGTATACATTGGAAGGTCCATTGCGTCTGCAACAGTCTTCTACCTTATTACA 612

DB 336 GGAATGATTTCCATTCACTGGAAGGTCCACTTCGACTCCAGCAGGCATATCTCATATG 395

QY 613 ATGCTGCACTAATGGCTCTGGTCTTTTATCAAGTACTACACAGAATGGAGTGTGTTT 672

DB 396 ATTAGTGCCCTCATGCCCCTGGTGTATATCAAGTACCTCCCTCAATGAGGACTGCGTCTC 455

QY 673 GTGCTGTTGTATCTCGGTTTGGGATCTGGTGTGCTGCTCACCACAAAGACCAATG 732

DB 456 ATCTTGGCTGTGATTTTCAGTATATGATTTAGGGGCTGTTTGTGTCGGAAGGTCCACTT 515

QY 733 AGATATTTGGTGAAGTTCACAGGAGAGAAACGACGCAATTTTCCCG 780

DB 516 CGTATGCTGGTGAACAGCTCAGGAGAGAAATGAACAGCTTTTCCAG 563

RESULT 50
AW367418
LOCUS
DEFINITION MR0-HT0164-211099-003-g03 HT0164 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW367418
VERSION AW367418.1 GI:6872068
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 553)
HGCP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&st2=MR0-HT0164-211099-003-g03&t3=1999-10-21&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 553.

FEATURES
source

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="HT0164"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
125 a 120 c 127 g 181 t

Query Match 12.6%; Score 189.4; DB 10; Length 553;
Best Local Similarity 61.0%; Pred. No. 2.7e-23;
Matches 307; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
Qy 289 GAACACACAGTATCGTTGAGAGGGATTGATGTCACCTTGAATGCTCTCGTCATCTTG 348
Db 50 GATACCGAGACTGTGGCCAGAGAGCCCTGACCTCAATCTGAATGCTGCCATCAGATC 109
Qy 349 TGGTGTGCTCTGTGACACAGTTCTGCTGATTTCTTCTATAAATACAAGTTTATAAG 408
Db 110 AGTGTCATTGTTGTCAGTACTATCTCTGCTGGTCTCTGTATAAATACAGTGCATAAG 169
Qy 409 CTATTTCATGGATGGCTTATTGTCAGCAGTTTCTTCTCTTTTCCTATTACTACATC 468
Db 170 GTCATCCATGCTGGTTTATTATATCATCTCTATGTTGCTGTTCTTTTTCATTTCATT 229
Qy 469 TATGTGCAAGAGTCTGAAAGTTTCGATGTCGTCTCCAGCGCACTATTGGTTTGT 528
Db 230 TACTTGGGGAAGTGTAAACCTATAACGTTGCTGTGGACTACATTACTGTGTGCACTC 289
Qy 529 GGACTGGGTAACTATGAGTTCTCGGAATGATGTATACATTGGAAGGTCCATTGCGT 588
Db 290 CTGATCTGGAATTGGGTGGTGGGAATGATTTCCATTACCTGGAAGGTCCACTTGA 349
Qy 589 CTGCAACAGTTCTACCTTATTACAATCTCTGCACATAATGGCTCTGGTCTTTATCAAGTAC 648

Db 350 CTCACAGCAGCATATCTCATTTAGTATGATAGTCCCTCATGGCCCTGGTGTATATCAAGTAC 409
Qy 649 CTACCAGAATGGACTGTGTGTTTGTCTGTTTGTATCTCGGTTTCGGATCTGGTGGCC 708
Db 410 CTCCTGAAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAAGTATATGATTTAGTGGCT 469
Qy 709 GTGCTCACACACAAAGACCATTTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAG 768
Db 470 GTTTGGTGTCCGAAACGCTCCACITTCGTATGCTGTGTTGAAACAGCTCAGGAGAAATGAA 529
Qy 769 CCAATTTTCCGGCGCTGATTTA 791
Db 530 ACGCTTTTCCAGCTCTCATTTA 552
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